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Identification of three QTLs with influence on susceptibility to helminth infections in pigs

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Intestinal helminth infections are causing health and welfare problems in both human and animal populations and among these also in pig production. A family, in which susceptibility towards *Ascaris* (large round worm) and *Trichuris* (whipworm) infections are segregating, was constructed. Our data demonstrate that genetic components are responsible for approximately 45% and 70% of the variation in *Ascaris* and *Trichuris* parasite loads, respectively. A genome scan using the Ilummina 7K SNP-chip has been performed in order to locate genomic regions controlling this susceptibility. A total of 194 pigs from 19 full-sib litters have been genotyped and 3955 informative SNPs were used to perform genotype association analysis. For *Trichuris* parasite load (faecal egg excretion) four SNPs in a 2 Mb region on SSC13 and 4 SNPs in a 7 Mb region on SSC11 have been identified, whereas 7 SNPs located within a 6 Mb region on SSC4 were associated with *Ascaris* egg excretion and worm load. The proportion of phenotypic variance accounted for by a SNP's genotype ranged from 0.08-0.14 and 0.06-0.12 for *Ascaris* and *Trichuris,* respectively. The next step is to verify the QTLs in an unrelated pig material and we are currently collecting samples for that purpose. After the validation we will resequence and annotate the QTL regions in both susceptible and resistant animals. Functional predictions of common genetic variation between susceptible and resistant animals will be made and these predictions will be used to